

D. Fitzgerald

#14
3F
6/26/00

1646

RAW SEQUENCE LISTING DATE: 05/31/2000
PATENT APPLICATION: US/09/039,177A TIME: 13:21:57

Input Set : A:\LUD5539.seq.txt
Output Set: N:\CRF3\05312000\I039177A.raw

ENTERED

C--> 3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: MIYAZONO, Kohei
6 IMAMURA, Takeshe
7 TEN DIJKE, Peter
9 (ii) TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE
10 KINASE DOMAINS, CORRESPONDING NUCLEIC
11 ACID MOLECULES, AND THEIR USE
13 (iii) NUMBER OF SEQUENCES: 29
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
17 (B) STREET: 666 Fifth Avenue
18 (C) CITY: New York City
19 (D) STATE: New York
20 (E) COUNTRY: USA
21 (F) ZIP: 10103
C--> 23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
25 (B) COMPUTER: IBM PS/2
26 (C) OPERATING SYSTEM: PC-DOS
27 (D) SOFTWARE: Wordperfect
C--> 29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/039,177A
C--> 31 (B) FILING DATE: 13-Mar-1998
32 (C) CLASSIFICATION: 435
67 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/436,265
36 (B) FILING DATE: October 30, 1995
39 (A) APPLICATION NUMBER: PCT/GB93/02367
40 (B) FILING DATE: November 17, 1993
43 (A) APPLICATION NUMBER: GB 9224057.1
44 (B) FILING DATE: November 17, 1992
47 (A) APPLICATION NUMBER: GB 9304677.9
48 (B) FILING DATE: March 8, 1993
51 (A) APPLICATION NUMBER: GB 9304680.3
52 (B) FILING DATE: March 8, 1993
55 (A) APPLICATION NUMBER: 9311047.6
56 (B) FILING DATE: May 28, 1993
60 (A) APPLICATION NUMBER: 9313763.6
61 (B) FILING DATE: July 2, 1993
64 (A) APPLICATION NUMBER: 9136099.2
65 (B) FILING DATE: August 3, 1993
68 (A) APPLICATION NUMBER: 321344.5
69 (B) FILING DATE: October 15, 1993
71 (viii) ATTORNEY/AGENT INFORMATION:
72 (A) NAME: Mary Anne Schofield
73 (B) REGISTRATION NUMBER: 36,669
74 (C) REFERENCE/DOCKET NUMBER: LUD 5539 - JEL/MAS

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76 (ix) TELECOMMUNICATION INFORMATION:
 77 (A) TELEPHONE: (212) 318-3000
 78 (B) TELEFAX: (212) 752-5958
 82 (2) INFORMATION FOR SEQ ID NO: 1:
 83 (i) SEQUENCE CHARACTERISTICS:
 84 (A) LENGTH: 1984 base pairs
 85 (B) TYPE: nucleic acid
 86 (C) STRANDEDNESS: unknown
 87 (D) TOPOLOGY: linear
 89 (ii) MOLECULE TYPE: cDNA
 91 (iii) HYPOTHETICAL: NO
 C--> 93 (iv) ANTI-SENSE: NO
 95 (v) FRAGMENT TYPE: internal
 97 (vi) ORIGINAL SOURCE:
 98 (A) ORGANISM: Homo sapiens
 100 (ix) FEATURE:
 101 (A) NAME/KEY: CDS
 102 (B) LOCATION: 283..1791
 104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 106 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
 108 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120
 110 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180
 112 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
 114 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294
 115 Met Thr Leu Gly
 116 1
 118 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
 119 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
 120 5 10 15 20
 122 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390
 123 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
 124 25 30 35
 126 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438
 127 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
 128 40 45 50
 130 GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486
 131 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
 132 55 60 65
 134 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
 135 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
 136 70 75 80
 138 GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
 139 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
 140 85 90 95 100
 142 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630
 143 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
 144 105 110 115
 146 GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG 678
 147 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu

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148				120					125				130				
150	GTG	GCC	CTG	GGT	GTC	CTG	GGC	CTG	TGG	CAT	GTC	CGA	CGG	AGG	CAG	GAG	726
151	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
152				135				140					145				
154	AAG	CAG	CGT	GGC	CTG	CAC	AGC	GAG	CTG	GGA	GAG	TCC	AGT	CTC	ATC	CTG	774
155	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
156				150			155						160				
158	AAA	GCA	TCT	GAG	CAG	GGC	GAC	ACG	ATG	TTG	GGG	GAC	CTC	CTG	GAC	AGT	822
159	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
160	165						170					175				180	
162	GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	CTG	GTG	CAG	AGG	870
163	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
164					185						190				195		
166	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC	918
167	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
168				200					205					210			
170	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	AGT	GTG	GCC	GTC	966
171	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
172				215				220					225				
174	AAG	ATC	TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	CGG	GAG	ACT	GAG	1014
175	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu	
176				230			235					240					
178	ATC	TAT	AAC	ACA	GTA	TTG	CTC	AGA	CAC	GAC	AAC	ATC	CTA	GGC	TTC	ATC	1062
179	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile	
180	245					250					255				260		
182	GCC	TCA	GAC	ATG	ACC	TCC	CGC	AAC	TCG	AGC	ACG	CAG	CTG	TGG	CTC	ATC	1110
183	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	
184					265					270				275			
186	ACG	CAC	TAC	CAC	GAG	CAC	GGC	TCC	CTC	TAC	GAC	TTT	CTG	CAG	AGA	CAG	1158
187	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Gln	Arg	Gln	
188				280				285						290			
190	ACG	CTG	GAG	CCC	CAT	CTG	GCT	CTG	AGG	CTA	GCT	GTG	TCC	GCG	GCA	TGC	1206
191	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys	
192				295				300					305				
194	GGC	CTG	GCG	CAC	CTG	CAC	GTG	GAG	ATC	TTC	GGT	ACA	CAG	GGC	AAA	CCA	1254
195	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	
196				310			315					320					
198																	

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214 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
215 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
216      390      395      400
218 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
219 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
220 405      410      415      420
222 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
223 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
224      425      430      435
226 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
227 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
228      440      445      450
230 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
231 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
232      455      460      465
234 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
235 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
236 470      475      480
238 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
239 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
240 485      490      495      500
242 GTG ATT CAA TAGCCACAGGA GCACCTGATT CCTTCTTGCC TGCAGGGGGC      1831
243 Val Ile Gln
245 TGGGGGGGTG GGGGGCAGTG GATGGTGGCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG      1891
247 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCACCC AGCCAAAAAT      1951
249 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA      1984
252 (2) INFORMATION FOR SEQ ID NO: 2:
253 (i) SEQUENCE CHARACTERISTICS:
254 (A) LENGTH: 503 amino acids
255 (B) TYPE: amino acid
256 (D) TOPOLOGY: linear
258 (ii) MOLECULE TYPE: protein
260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
262 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
263 1      5      10      15
265 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
266      20      25      30
268 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
269      35      40      45
271 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
272      50      55      60
274 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
275 65      70      75      80
277 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
278      85      90      95
280 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
281      100      105      110
283 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
284      115      120      125

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286 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
287      130      135      140
289 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
290 145      150      155      160
292 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
293      165      170      175
295 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
296      180      185      190
298 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
299      195      200      205
301 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
302      210      215      220
304 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
305 225      230      235      240
307 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
308      245      250      255
310 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
311      260      265      270
313 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
314      275      280      285
316 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
317      290      295      300
319 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
320 305      310      315      320
322 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
323      325      330      335
325 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
326      340      345      350
328 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
329      355      360      365
331 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
332      370      375      380
334 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
335 385      390      395      400
337 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
338      405      410      415
340 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
341      420      425      430
343 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
344      435      440      445
346 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
347      450      455      460
349 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
350 465      470      475      480
352 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
353      485      490      495
355 Glu Lys Pro Lys Val Ile Gln
356      500
359 (2) INFORMATION FOR SEQ ID NO: 3:

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VERIFICATION SUMMARY

DATE: 05/31/2000

PATENT APPLICATION: US/09/039,177A

TIME: 13:21:58

Input Set : A:\LUD5539.seq.txt

Output Set: N:\CRF3\05312000\I039177A.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:23 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:93 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:370 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:674 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:993 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1282 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1569 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1844 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2135 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2418 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2693 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2711 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2729 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2747 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2765 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2783 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2801 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26